Amendments to the Claims:

Please replace all prior versions of claims in the application with the following claim listing:

- 1-33. (Canceled)
- 34. (Previously presented) A method for detecting a PXE mutation in a patient by establishing if a mutation in an MRP6 gene is associated with PXE, the method comprising the steps of:
 - a) interrogating an MRP6 nucleic acid in a patient sample for the presence of a mutation;
 - b) if present, determining if the mutation is a co-segregator with a PXE phenotype; and
 - c) identifying said patient as having a PXE mutation if a mutation is present in said MRP6 nucleic acid and the mutation is a co-segregator with said PXE phenotype.
- 35. (Previously presented) The method according to claim 34, wherein the said patient sample is selected from the group consisting of blood, saliva, amniotic fluid, and tissue.
- 36. (Previously presented) The method according to claim 35, wherein the said patient sample is blood.
- 37. (Previously presented) The method according to claim 34 wherein said step a) comprises performing a nucleic acid sequence scanning assay.
- 38. (Previously presented) The method according to claim 37, wherein said scanning assay is selected from the group consisting of SSCP, DGGE, RFLP, LCR, DHPLC, and enzymatic cleavage.
- 39. (Previously presented) The method according to claim 34, wherein said step a) comprises a specific mutation detection assay.

- 40. (Previously presented) The method according to claim 39, wherein said detection assay is selected from the group consisting of oligonucleotide hybridization and primer extension assays.
- 41. (Previously presented) The method according to claim 34, wherein said step a) comprises a nucleic acid sequencing assay.
- 42. (Previously presented) The method according to claim 41, wherein said assay detects the presence of a mutation selected from the group consisting of a deletion, a substitution, an insertion, and a rearrangement.
- 43. (Previously presented) The method according to claim 34, wherein said mutation is a non-conserved amino acid substitution.
- 44. (Previously presented) The method according to claim 34, wherein said mutation is in a splice site in an intron.
- 45. (Previously presented) The method according to claim 34, wherein said mutation is in the promoter region of the MRP6 gene.
- 46. (Previously presented) The method according to claim 34, wherein said mutation is in a polyA site of the MRP6 gene
- 47. (Previously presented) The method according to claim 34, wherein said mutation is in an exon of the MRP6 gene.
- 48. (Previously presented) The method according to claim 47, wherein said exon is selected from exons 1-31 of the MRP6 gene
- 49. (Previously presented) The method according to claim 34, wherein said nucleic acid is selected from the group consisting of mRNA, genomic DNA, and cDNA.
- 50. (Previously presented) The method according to claim 34, wherein said step a) comprises a hybridization assay.

- 51. (Previously presented) The method according to claim 34, wherein said step b) comprises screening the mutation against a control panel of MRP6 genes isolated from normal individuals.
- 52. (Previously presented) The method according to claim 34, wherein said step b) comprises comparing the mutation with a list of known PXE mutations.
- 53. (Previously presented) The method according to claim 34, wherein the said PXE phenotype comprises a skin manifestation.
- 54. (Previously presented) The method according to claim 53, wherein the said skin manifestation comprises a skin lesion found in at least one of the areas in the group consisting of face, neck, axilla, antecubital fossa, popliteal fossa, groin and periumbilical.
- 55. (Previously presented) The method according to claim 53, wherein the said skin manifestation comprises a laxity and a loss of elasticity of the skin found in at least one of the areas in the group consisting of face, neck, axilla, antecubital fossa, popliteal fossa, groin and periumbilical.
- 56. (Previously presented) The method according to claim 53, wherein the said skin manifestation comprises the calcification of fragmented elastic fibers in the mid- and lower dermis.
- 57. (Previously presented) The method according to claim 34, wherein said PXE phenotype is an ocular manifestation.
- 58. (Previously presented) The method according to claim 57, wherein said ocular manifestation comprises at least one of the group consisting of retinal hemorrhage; angloid streaks; and the accumulation of abnormal elastic fibers in the Bruch's membrane.
- 59. (Previously presented) The method according to claim 34, wherein said PXE phenotype comprises a cardiovascular manifestation.

- 60. (Previously presented) The method according to claim 59, wherein said cardiovascular manifestation comprises at least one of the group consisting of premature atherosclerotic changes; intimal fibroplasia; early myocardial infarction; fibrous thickening of the endocardium; fibrous thickening of the atrioventricular valves; and atrial septal aneurysm.
- 61. (Previously presented) The method according to claim 34, wherein said PXE phenotype comprises gastrointestinal bleeding.
- 62. (Previously presented) The method according to claim 34, wherein said PXE phenotype comprises the mineralization of the elastic fibers in at least one of the group consisting of skin; arteries; and retina.
- 63. (Previously presented) A method for screening a patient for the presence of a PXE mutation, the method comprising the steps of:
 - a) interrogating an MRP6 nucleic acid in a patient sample for the presence of a mutation known to be a co-segregator with a PXE phenotype; and
 - b) identifying said patient as having a PXE mutation if the mutation from step a) is detected in said MRP6 nucleic acid.
- 64. (Previously presented) The method according to claim 63, wherein said mutation is a mutation in codon 1141.
- 65. (Previously presented) The method according to claim 63, wherein said mutation is a deletion of base 3775.
- 66. (Previously presented) The method according to claim 63, wherein said mutation is in a codon selected from the group consisting of 1114, 1138, 1141, 1298, 1302, 1303, 1314, and 1321.
- 67. (Previously presented) A method for identifying a patient at risk of having children with PXE, the method comprising the steps of:
 - a) interrogating an MRP6 nucleic acid in a patient sample for the presence of an MRP6 allele known to be a co-segregator with a PXE phenotype; and

- b) identifying said patient as being at risk of having children with PXE if the allele from step a) is detected in said MRP6 nucleic acid.
- 68. (Previously presented) A method for identifying a patient at risk of developing a PXE associated symptom, the method comprising the steps of:
 - a) interrogating an MRP6 nucleic acid in a patient sample for the presence of an MRP6 allele known to be a co-segregator with a PXE phenotype; and
 - b) identifying said patient as being at risk of developing a PXE associated symptom if the allele from step a) is detected in said MRP6 nucleic acid.
- 69. (Previously presented) The method according to claim 68, wherein said PXE associated symptom is cardiovascular disease.
- 70. (Previously presented) The method according to claim 68, wherein said PXE associated symptom is macular degeneration.
- 71. (Previously presented) A method for diagnosing PXE in a patient, the method comprising the steps of:
 - a) interrogating an MRP6 nucleic acid in a patient sample for the presence of a pair of two MRP6 alleles the pair known to co-segregate with a PXE phenotype; and
 - b) diagnosing said patient as having PXE if the pair of alleles from step a) are detected in said MRP6 nucleic acid.
- 72. (Previously presented) The method of claim 71, wherein said patient is a homozygous PXE patient.

- 73. (New) A method for testing a patient for the presence of a PXE mutation, the method comprising the steps of:
 - a) interrogating a patient sample for a mutation shown to be associated with PXE, the mutation being in the MRP6 gene, and the mutation is selected from the group consisting of:
 - i) at codon 1114, nucleotide 3341G>C;
 - ii) at codon 1138, nucleotide 3413G>A;
 - iii) at codon 1141, nucleotide 3421C>T;
 - iv) at codon 1259, nucleotide 3775delT;
 - v) at codon 1298, nucleotide 3892G>T;
 - vi) at codon 1302, nucleotide 3904G>A;
 - vii) at codon 1303, nucleotide 3907G>C;
 - viii) at codon 1314, nucleotide 3940C>T; and
 - ix) at codon 1321, nucleotide 3961G>A; and
 - b) identifying the patient as having a PXE mutation if the mutation from step a) is detected in the MRP6 gene.
- 74. (New) A method for testing a patient for the presence of a PXE mutation, the method comprising the steps of:
 - a) interrogating an MRP6 nucleic acid in a patient sample for the presence of a mutation shown to be associated with PXE, wherein the mutation is selected from the group consisting of:
 - i) at codon 518, nucleotide 1553 G>A; and
 - ii) a 16.5 kb deletion between exon 22 and exon 29 of the MRP6 nucleic acid; and

- b) identifying said patient as having a PXE mutation if the mutation from step a) is detected in said MRP6 nucleic acid.
- 75. (New) A method for identifying a PXE associated mutation in a patient, the method comprising the steps of:
 - a) interrogating an MRP6 nucleic acid in a patient sample for the presence of a mutation, wherein the mutation is selected from the group consisting of:
 - (i) a nonsense mutation, and
 - (ii) a frameshift mutation; and
 - b) identifying a PXE associated mutation in the patient if a mutation from step a) is detected in the MRP6 nucleic acid.
- 76. (New) The method of claim 75, wherein the mutation is detected in exons 1-29 of the MRP6 nucleic acid.
- 77. (New) The method of claim 75, wherein the nonsense mutation is detected in exons 1-24 of the MRP6 nucleic acid.
- 78. (New) The method of claim 75, wherein the frameshift mutation is detected in exons 1-27.